

SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: THE ROCKEFELLER UNIVERSITY
- (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Klauber & Jackson
  - (B) STREET: 411 Hackensack Avenue
  - (C) CITY: Hackensack
  - (D) STATE: New Jersey
  - (E) COUNTRY: USA
  - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/347,563
  - (B) FILING DATE: November 30, 1994
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/292,345
  - (B) FILING DATE: August 17, 1994
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Jackson Esq., David A.
  - (B) REGISTRATION NUMBER: 26,742
  - (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 201 487-5800
  - (B) TELEFAX: 201 343-1684
  - (C) TELEX: 133521

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2793 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
  - (A) DESCRIPTION: Murine ob cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Murine

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 57..560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|   |     |
|---|-----|
| GGATCCCTGC TCCAGCAGCT GCAAGGTGCA AGAAGAAGAA GATCCCAGGG AGGAAA   | 56  |
| ATG TGC TGG AGA CCC CTG TGT CGG TTC CTG TGG CTT TGG TCC TAT CTG | 104 |
| Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu |     |
| 1 5 10 15   |     |
| TCT TAT GTT CAA GCA GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA | 152 |
| Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys |     |
| 20 25 30  |     |
| ACC CTC ATC AAG ACC ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG | 200 |
| Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr |     |
| 35 40 45  |     |
| CAG TCG GTA TCC GCC AAG CAG AGG GTC ACT GGC TTG GAC TTC ATT CCT | 248 |
| Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro |     |
| 50 55 60  |     |
| GGG CTT CAC CCC ATT CTG AGT TTG TCC AAG ATG GAC CAG ACT CTG GCA | 296 |
| Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala |     |
| 65 70 75 80   |     |
| GTC TAT CAA CAG GTC CTC ACC AGC CTG CCT TCC CAA AAT GTG CTG CAG | 344 |
| Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln |     |
| 85 90 95  |     |
| ATA GCC AAT GAC CTG GAG AAT CTC CGA GAC CTC CTC CAT CTG CTG GCC | 392 |
| Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala |     |
| 100 105 110   |     |
| TTC TCC AAG AGC TGC TCC CTG CCT CAG ACC AGT GGC CTG CAG AAG CCA | 440 |
| Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro |     |
| 115 120 125   |     |
| GAG AGC CTG GAT GGC GTC CTG GAA GCC TCA CTC TAC TCC ACA GAG GTG | 488 |
| Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val |     |
| 130 135 140   |     |
| GTG GCT TTG AGC AGG CTG CAG GGC TCT CTG CAG GAC ATT CTT CAA CAG | 536 |
| Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln |     |
| 145 150 155 160   |     |
| TTG GAT GTT AGC CCT GAA TGC TGA AGTTTCAAAG GCCACCAGGC TCCCAAGA  | 588 |
| Leu Asp Val Ser Pro Glu Cys                                     |     |
| 165   |     |

|   |      |
|---|------|
| ATCATGTAGA GGGAAGAAAC CTTGGCTTCC AGGGGTCTTC AGGAGAAGAG AGCCATGTGC   | 648  |
| ACACATCCAT CATTCATTTT TCTCCCTCCT GTAGACCACC CATCCAAAGG CATGACTCCA   | 708  |
| CAATGCTTGA CTCAAGTTAT CCACACAAC T CATGAGCAC AAGGAGGGGC CAGCCTGCAG   | 768  |
| AGGGGACTCT CACCTAGTTC TTCAGCAAGT AGAGATAAGA GCCATCCCAT CCCCTCCATG   | 828  |
| TCCCACCTGC TCCGGGTACA TGTTCCTCCG TGGGTACACG CTTGCTGCG GCCCAGGAGA    | 888  |
| GGTGAGGTAG GGATGGGTAG AGCCTTTGGG CTGTCTCAGA GTCTTTGGGA GCACCGTGAA   | 948  |
| GGCTGCATCC ACACACAGCT GGAAACTCCC AAGCAGCACA CGATGGAAGC ACTTATTTAT   | 1008 |
| TTATTCTGCA TTCTATTTTG GATGGATCTG AAGCAAGGCA TCAGCTTTTT CAGGCTTTGG   | 1068 |
| GGGTCAGCCA GGATGAGGAA GGCTCCTGGG GTGCTGCTTT CAATCCTATT GATGGGTCTG   | 1128 |
| CCCGAGGCAA ACCTAATTTT TGAGTGACTG GAAGGAAGGT TGGGATCTTC CAAACAAGAG   | 1188 |
| TCTATGCAGG TAGCGCTCAA GATTGACCTC TGGTGACTGG TTTTGTTTCT ATTGTGACTG   | 1248 |
| ACTCTATCCA AACACGTTTG CAGCGGCATT GCCGGGAGCA TAGGCTAGGT TATTATCAAA   | 1308 |
| AGCAGATGAA TTTTGTCAAG TGTAATATGT ATCTATGTGC ACCTGAGGGT AGAGGATGTG   | 1368 |
| TTAGAGGGAG GGTGAAGGAT CCGGAAGTGT TCTCTGAATT ACATATGTGT GGTAGGCTTT   | 1428 |
| TCTGAAAGGG TGAGGCATTT TCTTACCTCT GTGGCCACAT AGTGTGGCTT TGTGAAAAGG   | 1488 |
| ACAAAGGAGT TGA CTCTTTC CGGAACATTT GGAGTG TACC AGGCACCCTT GGAGGGGCTA | 1548 |
| AAGCTACAGG CCTTTTGTTG GCATATTGCT GAGCTCAGGG AGTGAGGGCC CCACATTTGA   | 1608 |
| GACAGTGAGC CCCAAGAAAA GGGTCCCTGG TGTAGATCTC CAAGGTTGTC CAGGGTTGAT   | 1668 |
| CTCACAATGC GTTCTTAAG CAGGTAGACG TTTGCATGCC AATATGTGGT TCTCATCTGA    | 1728 |
| TTGGTTCATC CAAAGTAGAA CCCTGTCTCC CACCCATTCT GTGGGGAGTT TTGTTCCAGT   | 1788 |
| GGGAATGAGA AATCACTTAG CAGATGGTCC TGAGCCCTGG GCCAGCACTG CTGAGGAAGT   | 1848 |
| GCCAGGGCCC CAGGCCAGGC TGCCAGAATT GCCCTTCGGG CTGGAGGATG AACAAAGGGG   | 1908 |
| CTTGGGTTTT TCCATCACCC CTGCACCCTA TGTCACCATC AACTGGGGG GCAGATCAGT    | 1968 |
| GAGAGGACAC TTGATGGAAA GCAATACACT TTAAGACTGA GCACAGTTTC GTGCTCAGCT   | 2028 |
| CTGTCTGGTG CTGTGAGCTA GAGAAGCTCA CCACATACAT ATAAAAATCA GAGGCTCATG   | 2088 |
| TCCCTGTGGT TAGACCCTAC TCGCGGCGGT GTACTCCACC ACAGCAGCAC CGCACCGCTG   | 2148 |
| GAAGTACAGT GCTGTCTTCA ACAGGTGTGA AAGAACCTGA GCTGAGGGTG ACAGTGCCCA   | 2208 |
| GGGGAACCTT GCTTGCACTC TATTGCATTT ACATACCGCA TTTCAGGGCA CATTAGCATC   | 2268 |
| CACTCCTATG GTAGCACACT GTTGACAATA GGACAAGGGA TAGGGGTTGA CTATCCCTTA   | 2328 |

|   |      |
|---|------|
| TCCAAAATGC TTGGGACTAG AAGAGTTTGG GATTTTAGAG TCTTTTCAGG CATAGGTATA | 2388 |
| TTTGAGTATA TATAAAATGA GATATCTTGG GGATGGGGCC CAAGTATAAA CATGAAGTTC | 2448 |
| ATTTATATTT CATAATACCG TATAGACACT GCTTGAAGTG TAGTTTTATA CAGTGTMTTA | 2508 |
| AATAACGTTG TATGCATGAA AGACGTTTTT ACAGCATGAA CCTGTCTACT CATGCCAGCA | 2568 |
| CTCAAAAACC TTGGGGTTTT GGAGCAGTTT GGATCTTGGG TTTTCTGTTA AGAGATGGTT | 2628 |
| AGCTTATACC TAAACCATA ATGGCAAACA GGCTGCAGGA CCAGACTGGA TCCTCAGCCC  | 2688 |
| TGAAGTGTGC CCTTCCAGCC AGGTCATACC CTGTGGAGGT GAGCGGGATC AGGTTTTGTG | 2748 |
| GTGCTAAGAG AGGAGTTGGA GGTAGATTTT GGAGGATCTG AGGGC                 | 2793 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Murine ob polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Trp | Arg | Pro | Leu | Cys | Arg | Phe | Leu | Trp | Leu | Trp | Ser | Tyr | Leu | 1   | 5   | 10  | 15  |
| Ser | Tyr | Val | Gln | Ala | Val | Pro | Ile | Gln | Lys | Val | Gln | Asp | Asp | Thr | Lys | 20  | 25  | 30  |     |
| Thr | Leu | Ile | Lys | Thr | Ile | Val | Thr | Arg | Ile | Asn | Asp | Ile | Ser | His | Thr | 35  | 40  | 45  |     |
| Gln | Ser | Val | Ser | Ala | Lys | Gln | Arg | Val | Thr | Gly | Leu | Asp | Phe | Ile | Pro | 50  | 55  | 60  |     |
| Gly | Leu | His | Pro | Ile | Leu | Ser | Leu | Ser | Lys | Met | Asp | Gln | Thr | Leu | Ala | 65  | 70  | 75  | 80  |
| Val | Tyr | Gln | Gln | Val | Leu | Thr | Ser | Leu | Pro | Ser | Gln | Asn | Val | Leu | Gln | 85  | 90  | 95  |     |
| Ile | Ala | Asn | Asp | Leu | Glu | Asn | Leu | Arg | Asp | Leu | Leu | His | Leu | Leu | Ala | 100 | 105 | 110 |     |
| Phe | Ser | Lys | Ser | Cys | Ser | Leu | Pro | Gln | Thr | Ser | Gly | Leu | Gln | Lys | Pro | 115 | 120 | 125 |     |
| Glu | Ser | Leu | Asp | Gly | Val | Leu | Glu | Ala | Ser | Leu | Tyr | Ser | Thr | Glu | Val | 130 | 135 | 140 |     |
| Val | Ala | Leu | Ser | Arg | Leu | Gln | Gly | Ser | Leu | Gln | Asp | Ile | Leu | Gln | Gln | 145 | 150 | 155 | 160 |

Leu Asp Val Ser Pro Glu Cys  
165

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (A) DESCRIPTION: Human ob cDNA where N represents any nucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 46..546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|   |     |
|---|-----|
| NNNGNNGTTG CAAGGCCCAA GAAGCCCANN NTCCTGGGAA GGAAA ATG CAT TGG   | 54  |
| Met His Trp   |     |
| 1   |     |
| GGA ACC CTG TGC GGA TTC TTG TGG CTT TGG CCC TAT CTT TTC TAT GTC | 102 |
| Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu Phe Tyr Val |     |
| 5 10 15   |     |
| CAA GCT GTG CCC ATC CAA AAA GTC CAA GAT GAC ACC AAA ACC CTC ATC | 150 |
| Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile |     |
| 20 25 30 35   |     |
| AAG ACA ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG CAG TCA GTC | 198 |
| Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val |     |
| 40 45 50  |     |
| TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC CAC | 246 |
| Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His |     |
| 55 60 65  |     |
| CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC CAA | 294 |
| Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln |     |
| 70 75 80  |     |
| CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC AAC | 342 |
| Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn |     |
| 85 90 95  |     |

|   |     |
|---|-----|
| GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT AAG   | 390 |
| Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys   |     |
| 100 105 110 115   |     |
| AGC TGC CAC TTG CCC TGG GCC AGT GGC CTG GAG ACC TTG GAC AGC CTG   | 438 |
| Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu   |     |
| 120 125 130   |     |
| GGG GGT GTC CTG GAA GCT TCA GGC TAC TCC ACA GAG GTG GTG GCC CTG   | 486 |
| Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu   |     |
| 135 140 145   |     |
| AGC AGG CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC CTC   | 534 |
| Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu   |     |
| 150 155 160   |     |
| AGC CCT GGG TGC TGAGGCCTT GAAGGTCACT CTTCTGCAA GGACTNACGT         | 585 |
| Ser Pro Gly Cys   |     |
| 165   |     |
| TAAGGGAAGG AACTCTGGTT TCCAGGTATC TCCAGGATTG AAGAGCATTG CATGGACACC | 645 |
| CCTTATCCAG GACTCTGTCA ATTTCCCTGA CTCCTCTAAG CCACTCTTCC AAAGG      | 700 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Human ob polypeptide

(vi) ORIGINAL SOURCE: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|   |  |
|---|--|
| Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu |  |
| 1 5 10 15   |  |
| Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys |  |
| 20 25 30  |  |
| Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr |  |
| 35 40 45  |  |
| Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro |  |
| 50 55 60  |  |
| Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala |  |
| 65 70 75 80   |  |
| Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln |  |
| 85 90 95  |  |
| Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala |  |

100

105

110

Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu  
 115 120 125

Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val  
 130 135 140

Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln  
 145 150 155 160

Leu Asp Leu Ser Pro Gly Cys  
 165

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: Murine ob polypeptide lacking Gln at position 49

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu  
 1 5 10 15  
 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys  
 20 25 30  
 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr  
 35 40 45  
 Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly  
 50 55 60  
 Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val  
 65 70 75 80  
 Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile  
 85 90 95  
 Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe  
 100 105 110  
 Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu  
 115 120 125

Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val  
 130 135 140

Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu  
 145 150 155 160

Asp Val Ser Pro Glu Cys  
 165

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) Description: Human ob polypeptide lacking Gln at position 49

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu  
 1 5 10 15

Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys  
 20 25 30

Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr  
 35 40 45

Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly  
 50 55 60

Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val  
 65 70 75 80

Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile  
 85 90 95

Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe  
 100 105 110

Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp  
 115 120 125

Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val  
 130 135 140

Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu  
 145 150 155 160

Asp Leu Ser Pro Gly Cys  
 165



(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: exon 2G7

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|   |     |
|---|-----|
| GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTGCTG GAGACCCCTG TGTCGGGTCC | 60  |
| NGTGGNTTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC TATCCAGAAA GTCCAGGATG | 120 |
| ACACCAAAAAG CCTCATCAAG ACCATTGTCA NCAGGATCAC TGANATTTCAC CACACG   | 176 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: PCR 5' primer for exon 2G7

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCAGGGCAGG AAAATGTG

18

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: PCR 3' primer for exon 2G7

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATCCTGGAC TTTCTGGATA GG

22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: putative N-terminal signal peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu  
1                      5                      10                      15

Ser Tyr Val Gln Ala Val Pro  
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (plasmid)

(A) DESCRIPTION: pET-15b expression vector

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: T7 promoter

(B) LOCATION: 20..37

(ix) FEATURE:

(A) NAME/KEY: lac operator

(B) LOCATION: 39..64

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 108..243

(ix) FEATURE:

(A) NAME/KEY: His-Tag

(B) LOCATION: 123..137

(ix) FEATURE:

(A) NAME/KEY: Thrombin cleavage site

(B) LOCATION: 184..196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA      60
TCCCCCTCTA CAAATAATTT TGTTTAACTT TAAGAAGGAG ATATAACC ATG GGC AGC      116
                                     Met Gly Ser
                                     1
AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG CGC GGC AGC      164
Ser His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
   5                10                15
CAT ATG CTC GAG GAT CCC GCT GCT AAC AAA GCC CGA AAG GAA GCT GAG      212
His Met Leu Glu Asp Pro Ala Ala Asn Lys Ala Arg Lys Glu Ala Glu
   20                25                30                35
TTG GCT GCT GCC ACC GCT GAG CAA TAA CTA G CATAACCCCT TGGGGCCTCT      263
Leu Ala Ala Ala Thr Ala Glu Gln *
               40
AAACGGGTCT TGAGGGGTTT TTTG      287
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
   1                5                10                15
Arg Gly Ser His Met Leu Glu Asp Pro Ala Ala Asn Lys Ala Arg Lys
               20                25                30
Glu Ala Glu Leu Ala Ala Ala Thr Ala Glu Gln
   35                40
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: Murine 5' primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTATGTTCA TATGGTGCCG ATCCAGAAAG TC

32

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Murine 3' primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCCCTCTACA TATGTCTTGG GAGCCTGGTG GC

32

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: Human 5' primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCTATGTCCA TATGGTGCCG ATCCAAAAAG TC

32

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: Human 3' primer

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTCCTTCCCA TATGGTACTC CTTGCAGGAA GA

32

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (A) DESCRIPTION: Splice acceptor site in ob

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: Splice acceptor site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCAGTCGGT A

11

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

- (A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr  
1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala  
1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
(A) DESCRIPTION: ob peptide fragment

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu  
1                      5                      10                      15

Ser Leu Asp

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
  - (A) DESCRIPTION: ob peptide fragment
- (v) FRAGMENT TYPE: Carboxyl terminal
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val
1           5           10           15
Ser Pro Glu Cys
                20

```

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 414 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
  - (A) DESCRIPTION: portion of the human ob gene including noncoding sequence upstream of first exon, coding sequence of first exon, and 5' region of first intron
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 38..181
- (ix) FEATURE:
  - (A) NAME/KEY: 5' region of first intron
  - (B) LOCATION: 182..414
- (ix) FEATURE:
  - (A) NAME/KEY: 5' noncoding sequence of the human ob gene from which the HOB 1gF DNA primer was generated
  - (B) LOCATION: 11..28
- (ix) FEATURE:
  - (A) NAME/KEY: intronic sequence of the human ob gene from which the HOB 1gR primer was generated

(B) LOCATION: 241..260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|            |            |            |            |            |            |     |     |     |     |            |     |
|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|------------|-----|
| GGTTGCAAGG | CCCAAGAAGC | CCATCCTGGG | AAGGAAA    | ATG        | CAT        | TGG | GGA | ACC | CTG |            | 55  |
|            |            |            |            | Met        | His        | Trp | Gly | Thr | Leu |            |     |
|            |            |            |            | 1          |            |     |     | 5   |     |            |     |
| TGC        | GGA        | TTC        | TTG        | TGG        | CTT        | TGG | CCC | TAT | CTT | TTC        | 103 |
| Cys        | Gly        | Phe        | Leu        | Trp        | Leu        | Trp | Pro | Tyr | Leu | Phe        |     |
|            |            |            | 10         |            |            |     | 15  |     |     |            |     |
|            |            |            |            |            |            |     |     |     |     | 20         |     |
| CCC        | ATC        | CAA        | AAA        | GTC        | CAA        | GAT | GAC | ACC | AAA | ACC        | 151 |
| Pro        | Ile        | Gln        | Lys        | Val        | Gln        | Asp | Asp | Thr | Lys | Thr        |     |
|            |            |            | 25         |            |            |     | 30  |     |     |            |     |
|            |            |            |            |            |            |     |     |     |     | 35         |     |
| GTC        | ACC        | AGG        | ATC        | AAT        | GAC        | ATT | TCA | CAC | ACG | GTAAGGAGAG | 201 |
| Val        | Thr        | Arg        | Ile        | Asn        | Asp        | Ile | Ser | His | Thr |            |     |
|            |            |            | 40         |            |            |     | 45  |     |     |            |     |
| CAAAGTAGAA | CTGCAGCCAG | CCCAGCACTG | GCTCCTAGTG | GCACTGGACC | CAGATAGTCC |     |     |     |     |            | 261 |
| AAGAAACATT | TATTGAACGC | CTCCTGAATG | CCAGGCACCT | ACTGGAAGCT | GAGAAGGATT |     |     |     |     |            | 321 |
| TTGGATAGCA | CAGGGCTCCA | CTCTTTCTGG | TTGTTTCTTN | TGGCCCCCTC | TGCCTGCTGA |     |     |     |     |            | 381 |
| GATNCCAGGG | GTTAGNGGTT | CTTAATTCCT | AAA        |            |            |     |     |     |     |            | 414 |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: N-terminal portion of the human ob protein encoded by first exon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | His | Trp | Gly | Thr | Leu | Cys | Gly | Phe | Leu | Trp | Leu | Trp | Pro | Tyr | Leu |  |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |  |
| Phe | Tyr | Val | Gln | Ala | Val | Pro | Ile | Gln | Lys | Val | Gln | Asp | Asp | Thr | Lys |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |  |
| Thr | Leu | Ile | Lys | Thr | Ile | Val | Thr | Arg | Ile | Asn | Asp | Ile | Ser | His | Thr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: portion of the human ob gene including 3' region of first intron, coding sequence of second exon, and 3' noncoding sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 291..648

(ix) FEATURE:

(A) NAME/KEY: 3' of first intron

(B) LOCATION: 1..290

(ix) FEATURE:

(A) NAME/KEY: intronic sequence of the human ob gene HOB from which the HOB 2gF primer was generated

(B) LOCATION: 250..269

(ix) FEATURE:

(A) NAME/KEY: 3' noncoding sequence of the human ob gene from which the HOB 2gR DNA primer was generated

(B) LOCATION: 707..728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|   |         |
|---|---------|
| CTGGTTCTTT CAGGAAGAGG CCATGTAAGA GAAAGGAATT GACCTAGGGA AAATTGGCCT | 60      |
| GGGAAGTGGA GGAACGGAT GGTGTGGGAA AAGCAGGAAT CTCGGAGACC AGCTTAGAGG  | 120     |
| CTTGGCAGTC ACCTGGGTGC AGGANACAAG GGCCTGAGCC AAAGTGGTGA GGGAGGGTGG | 180     |
| AAGGAGACAG CCCAGAGAAT GACCCTCCAT GCCCACGGGG AAGGCAGAGG GCTCTGAGAG | 240     |
| CGATTCCTCC CACATGCTGA GCACTTGTTT TCCCTCTTCC TCCTNCATAG CAG TCA    | 296     |
|   | Gln Ser |
|   | 1       |
| GTC TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC   | 344     |
| Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu   |         |
| 5 10 15   |         |
| CAC CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC   | 392     |
| His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr   |         |
| 20 25 30  |         |
| CAA CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC   | 440     |
| Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser   |         |
| 35 40 45 50   |         |

|  |     |
|--|-----|
| AAC GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT<br>Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser | 488 |
| 55 60 65   |     |
| AAG AGC TGC CAC TTG CCC TGG GCC AGT GGC CTG GAG ACC TTG GAC AGC<br>Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser | 536 |
| 70 75 80   |     |
| CTG GGG GGT GTC CTG GAA GCT TCA GGC TAC TCC ACA GAG GTG GTG GCC<br>Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala | 584 |
| 85 90 95   |     |
| CTG AGC AGG CTG CAG GGG TCT CTG CAG GAC ATG CTG TGG CAG CTG GAC<br>Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp | 632 |
| 100 105 110  |     |
| CTC AGC CCT GGG TGC T GAGGCCTTGA AGGTCACTCT TCCTGCAAGG ACTACGTTAA<br>Leu Ser Pro Gly Cys   | 688 |
| 115  |     |
| GGGAAGGAAC TCTGGCTTTC CAGGTATCTC CAGGATTGAA GAGCATTGCA TGGACACCCC  | 748 |
| TTATCCAGGA CTCTGTCAAT TTCCCTGACT CCTCTAAGCC ACTCTTCCAA AGG   | 801 |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: C-terminal portion of the human ob protein encoded by second exon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|   |    |    |    |    |
|---|----|----|----|----|
| Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro | 1  | 5  | 10 | 15 |
| Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala | 20 | 25 | 30 |    |
| Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln | 35 | 40 | 45 |    |
| Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala | 50 | 55 | 60 |    |
| Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu | 65 | 70 | 75 | 80 |
| Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val | 85 | 90 | 95 |    |
| Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln |    |    |    |    |

Leu Asp Leu Ser Pro Gly Cys  
115

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: pichia yeast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Glu Lys Arg Glu Ala Glu Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: pichia yeast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Glu Ala Glu Ala  
1

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: Internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: pichia yeast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28: -

Leu Glu Lys Arg  
1

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: HOB 1gF DNA primer generated from the 5' noncoding sequence of the human ob gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCAAGAAGC CCATCCTG

18

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: HOB 1gR DNA primer generated from the first intronic sequence of the human ob gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GACTATCTGG GTCCAGTGCC

20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: HOB 2gF DNA primer generated from the first intronic sequence of the human ob gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCACATGCTG AGCACTTGTT

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)  
(A) DESCRIPTION: HOB 2gR DNA primer generated from the 3' noncoding sequence of the human ob gene

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTCAATCCT GGAGATACCT GG

22

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA  
(A) DESCRIPTION: pPIC.9 cloning site

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTCGAGAAAA GAGAGGCTGA AGCTTACGTA GAATTCCTTA GGCCGGCCGG G

51

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: PCR 5' primer for amplifying human ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTATCTCTCG AGAAAAGAGT GCCCATCCAA AAAGTCCAAG

40

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: PCR 3' primer for amplifying human ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCGCGAATTC TCAGCACCCA GGGCTGAGGT C

31

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

(A) DESCRIPTION: PCR 5' primer for amplifying murine ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTATCTCTCG AGAAAAGAGT GCCTATCCAG AAAGTCCAGG

40

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (A) DESCRIPTION: PCR 3' primer for amplifying murine ob cDNA sequence

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGCGAATTC TCAGCATTCA GGGCTAACAT C-

31

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: tetrapeptide at N-terminus of renatured murine ob protein after thrombin cleavage

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Murine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Ser His Met

1